

SEQUENCE LISTING

<110> Olandt, Peter J.
Meyers, Rachel E.
Galvin, Katherine A.
Millennium Pharmaceuticals Inc.

<120> 33945, A Human Glycosyltransferase and
Uses Therefor

<130> MPI2001-018P1RCP1(M)

<150> 60/269202
<151> 2001-02-15

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Met Trp Gly Arg Thr Ala Arg Arg Arg Cys Pro
1 5 10

cg gaa ctg cgg cgc ggc cgg gag gcg ctg ttg gtg ctc ctg gcg cta 161
Arg Glu Leu Arg Arg Gly Arg Glu Ala Leu Leu Val Leu Leu Ala Leu
15 20 25

ctg gcg ttg gcc ggg ctg ggc tcg gtg ctg cgg gcg cag cgt ggg gcc 209
Leu Ala Leu Ala Gly Leu Gly Ser Val Leu Arg Ala Gln Arg Gly Ala
30 35 40

ggg gcc ggg gct gcc gag ccg gga ccc ccg cgc acc ccg cgc ccc ggg 257
Gly Ala Gly Ala Ala Glu Pro Gly Pro Pro Arg Thr Pro Arg Pro Gly
45 50 55

ccg cgc gag ccg gtc atg ccg cgg ccg gtg ccc gcg aac gcg ctg 305
Arg Arg Glu Pro Val Met Pro Arg Pro Pro Val Pro Ala Asn Ala Leu
60 65 70 75

ggc gcg cgg ggc gag gcg gtg cgg ctg cag ctg cag ggc gag gag ctg 353
Gly Ala Arg Gly Glu Ala Val Arg Leu Gln Leu Gln Gly Glu Glu Leu
80 85 90

ccg ctg cag gag gag agc gtg cgg ctg cac cag att aac atc tac ctc 401
Arg Leu Gln Glu Glu Ser Val Arg Leu His Gln Ile Asn Ile Tyr Leu
95 100 105

agc gac cgc atc tca ctg cac cgc cgc ctg ccc gag cgc tgg aac ccg 449
Ser Asp Arg Ile Ser Leu His Arg Arg Leu Pro Glu Arg Trp Asn Pro

2008-07-25

110

115

120

ctg tgc aaa gag aag aaa tat gat tat gat aat ttg ccc agg aca tct Leu Cys Lys Glu Lys Lys Tyr Asp Tyr Asp Asn Leu Pro Arg Thr Ser 125	130	135	497
gtt atc ata gca ttt tat aat gaa gcc tgg tca act ctc ctt cg aca Val Ile Ile Ala Phe Tyr Asn Glu Ala Trp Ser Thr Leu Leu Arg Thr 140	145	150	545
gtt tac agt gtc ctt gag aca tcc ccg gat atc ctg cta gaa gaa gtg Val Tyr Ser Val Leu Glu Thr Ser Pro Asp Ile Leu Leu Glu Glu Val 160	165	170	593
atc ctt gta gat gac tac agt gat aga gag cac ctg aag gag cgc ttg Ile Leu Val Asp Asp Tyr Ser Asp Arg Glu His Leu Lys Glu Arg Leu 175	180	185	641
gcc aat gag ctt tcg gga ctg ccc aag gtg cgc ctg atc cgc gcc aac Ala Asn Glu Leu Ser Gly Leu Pro Lys Val Arg Leu Ile Arg Ala Asn 190	195	200	689
aag aga gag ggc ctg gtg cga gcc ccg ctg ctg ggg gcg tct gcg gcg Lys Arg Glu Gly Leu Val Arg Ala Arg Leu Leu Gly Ala Ser Ala Ala 205	210	215	737
agg ggc gat gtt ctg acc ttc ctg gac tgt cac tgt gag tgc cac gaa Arg Gly Asp Val Leu Thr Phe Leu Asp Cys His Cys Glu Cys His Glu 220	225	230	785
ggg tgg ctg gag ccg ctg cag agg atc cat gaa gag gag tcg gca Gly Trp Leu Glu Pro Leu Leu Gln Arg Ile His Glu Glu Ser Ala 240	245	250	833
gtg gtg tgc ccg gtg att gat gtg atc gac tgg aac acc ttc gaa tac Val Val Cys Pro Val Ile Asp Val Ile Asp Trp Asn Thr Phe Glu Tyr 255	260	265	881
ctg ggg aac tcc ggg gag ccc cag atc ggc ggt ttc gac tgg agg ctg Leu Gly Asn Ser Gly Glu Pro Gln Ile Gly Phe Asp Trp Arg Leu 270	275	280	929
gtg ttc acg tgg cac aca gtt cct gag agg gag agg ata cgg atg caa Val Phe Thr Trp His Thr Val Pro Glu Arg Glu Arg Ile Arg Met Gln 285	290	295	977
tcc ccc gtc gat gtc atc agg tct cca aca atg gct ggt ggg ctg ttt Ser Pro Val Asp Val Ile Arg Ser Pro Thr Met Ala Gly Gly Leu Phe 300	305	310	1025
gct gtg agt aag aaa tat ttt gaa tat ctg ggg tct tat gat aca gga Ala Val Ser Lys Lys Tyr Phe Glu Tyr Leu Gly Ser Tyr Asp Thr Gly 320	325	330	1073
atg gaa gtt tgg gga gga gaa aac ctc gaa ttt tcc ttt agg atc tgg Met Glu Val Trp Gly Gly Glu Asn Leu Glu Phe Ser Phe Arg Ile Trp 335	340	345	1121
cag tgt ggt ggg gtt ctg gaa aca cac cca tgt tcc cat gtt ggc cat Gln Cys Gly Gly Val Leu Glu Thr His Pro Cys Ser His Val Gly His 350	355	360	1169

2000-02-10

gtt ttc ccc aag caa gct ccc tac tcc cgc aac aag gct ctg gcc aac Val Phe Pro Lys Gln Ala Pro Tyr Ser Arg Asn Lys Ala Leu Ala Asn	365 370 375	1217
agt gtt cgt gca gct gaa gta tgg atg gat gaa ttt aaa gag ctc tac Ser Val Arg Ala Ala Glu Val Trp Met Asp Glu Phe Lys Glu Leu Tyr	380 385 390 395	1265
tac cat cgc aac ccc cgt gcc cgc ttg gaa cct ttt ggg gat gtg aca Tyr His Arg Asn Pro Arg Ala Arg Leu Glu Pro Phe Gly Asp Val Thr	400 405 410	1313
gag agg aag cag ctc cgg gac aag ctc cag tgt aaa gac ttc aag tgg Glu Arg Lys Gln Leu Arg Asp Lys Leu Gln Cys Lys Asp Phe Lys Trp	415 420 425	1361
ttc ttg gag act gtg tat cca gaa ctg cat gtg cct gag gac agg cct Phe Leu Glu Thr Val Tyr Pro Glu Leu His Val Pro Glu Asp Arg Pro	430 435 440	1409
ggc ttc ttc ggg atg ctc cag aac aaa gga cta aca gac tac tgc ttt Gly Phe Phe Gly Met Leu Gln Asn Lys Gly Leu Thr Asp Tyr Cys Phe	445 450 455	1457
gac tat aac cct ccc gat gaa aac cag att gtg gga cac cag gtc att Asp Tyr Asn Pro Pro Asp Glu Asn Gln Ile Val Gly His Gln Val Ile	460 465 470 475	1505
ctg tac ctc tgt cat ggg atg ggc cag aat cag ttt ttc gag tac acg Leu Tyr Leu Cys His Gly Met Gly Gln Asn Gln Phe Phe Glu Tyr Thr	480 485 490	1553
tcc cag aaa gaa ata cgc tat aac acc cac cag cct gag ggc tgc att Ser Gln Lys Glu Ile Arg Tyr Asn Thr His Gln Pro Glu Gly Cys Ile	495 500 505	1601
gct gtg gaa gca gga atg gat acc ctt atc atg cat ctc tgc gaa gaa Ala Val Glu Ala Gly Met Asp Thr Leu Ile Met His Leu Cys Glu Glu	510 515 520	1649
act gcc cca gag aat cag aag ttc atc ttg cag gag gat gga tct tta Thr Ala Pro Glu Asn Gln Lys Phe Ile Leu Gln Glu Asp Gly Ser Leu	525 530 535	1697
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agt gac agt ttc gtt cca ctc tta cga gac tgc acc aac tcg gat cat Ser Asp Ser Phe Val Pro Leu Leu Arg Asp Cys Thr Asn Ser Asp His	560 565 570	1793
cag aaa tgg ttc ttc aaa gag cgc atg tta tga agcctcggt atcaaggagc Gln Lys Trp Phe Phe Lys Glu Arg Met Leu *	575 580	1846
ccatcgaagg agactgtgga gccaggactc tgcccaacaa agacttagct aagcagtgac cagaaccac caaaaactag gctgcattgc tttgaagagg caatcatttt gccatttggt aaagttgtgt tggatTTAGT aaaaatgtga ataagcttt tacttatttt gagaactttt taaatgttcc aaaataccct atttcaaag ggtaatcgta agatgttaac ccttggattt		1906 1966 2026 2086

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<210> 2

<211> 581

<212> PRT

<213> homo sapiens

<400> 2

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							20			25				30	
Leu	Gly	Ser	Val	Leu	Arg	Ala	Gln	Arg	Gly	Ala	Gly	Ala	Gly	Ala	Ala
					35			40				45			
Glu	Pro	Gly	Pro	Pro	Arg	Thr	Pro	Arg	Pro	Gly	Arg	Arg	Glu	Pro	Val
					50			55			60				
Met	Pro	Arg	Pro	Pro	Val	Pro	Ala	Asn	Ala	Leu	Gly	Ala	Arg	Gly	Glu
					65			70			75			80	
Ala	Val	Arg	Leu	Gln	Leu	Gln	Gly	Glu	Glu	Leu	Arg	Leu	Gln	Glu	Glu
					85				90				95		
Ser	Val	Arg	Leu	His	Gln	Ile	Asn	Ile	Tyr	Leu	Ser	Asp	Arg	Ile	Ser
					100				105				110		
Leu	His	Arg	Arg	Leu	Pro	Glu	Arg	Trp	Asn	Pro	Leu	Cys	Lys	Glu	Lys
					115				120				125		
Lys	Tyr	Asp	Tyr	Asp	Asn	Leu	Pro	Arg	Thr	Ser	Val	Ile	Ile	Ala	Phe
					130				135				140		
Tyr	Asn	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	Val	Tyr	Ser	Val	Leu
					145				150			155			160
Glu	Thr	Ser	Pro	Asp	Ile	Leu	Leu	Glu	Glu	Val	Ile	Leu	Val	Asp	Asp
					165				170				175		
Tyr	Ser	Asp	Arg	Glu	His	Leu	Lys	Glu	Arg	Leu	Ala	Asn	Glu	Leu	Ser
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Gly	Leu	Pro	Lys	Val	Arg	Leu	Ile	Arg	Ala	Asn	Lys	Arg	Glu	Gly	Leu
					195				200			205			
Val	Arg	Ala	Arg	Leu	Leu	Gly	Ala	Ser	Ala	Ala	Arg	Gly	Asp	Val	Leu
					210				215			220			
Thr	Phe	Leu	Asp	Cys	His	Cys	Glu	Cys	His	Glu	Gly	Trp	Leu	Glu	Pro
					225				230			235			240
Leu	Leu	Gln	Arg	Ile	His	Glu	Glu	Glu	Ser	Ala	Val	Val	Cys	Pro	Val
					245				250				255		
Ile	Asp	Val	Ile	Asp	Trp	Asn	Thr	Phe	Glu	Tyr	Leu	Gly	Asn	Ser	Gly
					260				265			270			
Glu	Pro	Gln	Ile	Gly	Gly	Phe	Asp	Trp	Arg	Leu	Val	Phe	Thr	Trp	His
					275				280			285			
Thr	Val	Pro	Glu	Arg	Glu	Arg	Ile	Arg	Met	Gln	Ser	Pro	Val	Asp	Val
					290				295			300			
Ile	Arg	Ser	Pro	Thr	Met	Ala	Gly	Gly	Leu	Phe	Ala	Val	Ser	Lys	Lys
					305				310			315			320
Tyr	Phe	Glu	Tyr	Leu	Gly	Ser	Tyr	Asp	Thr	Gly	Met	Glu	Val	Trp	Gly

2002-4-26 2002-4-26

2002-03-27 08:20:23

325	330	335
Gly Glu Asn Leu Glu Phe Ser Phe Arg Ile Trp Gln Cys Gly Gly Val		
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Leu Glu Thr His Pro Cys Ser His Val Gly His Val Phe Pro Lys Gln		
355	360	365
Ala Pro Tyr Ser Arg Asn Lys Ala Leu Ala Asn Ser Val Arg Ala Ala		
370	375	380
Glu Val Trp Met Asp Glu Phe Lys Glu Leu Tyr Tyr His Arg Asn Pro		
385	390	395
Arg Ala Arg Leu Glu Pro Phe Gly Asp Val Thr Glu Arg Lys Gln Leu		
405	410	415
Arg Asp Lys Leu Gln Cys Lys Asp Phe Lys Trp Phe Leu Glu Thr Val		
420	425	430
Tyr Pro Glu Leu His Val Pro Glu Asp Arg Pro Gly Phe Phe Gly Met		
435	440	445
Leu Gln Asn Lys Gly Leu Thr Asp Tyr Cys Phe Asp Tyr Asn Pro Pro		
450	455	460
Asp Glu Asn Gln Ile Val Gly His Gln Val Ile Leu Tyr Leu Cys His		
465	470	475
Gly Met Gly Gln Asn Gln Phe Phe Glu Tyr Thr Ser Gln Lys Glu Ile		
485	490	495
Arg Tyr Asn Thr His Gln Pro Glu Gly Cys Ile Ala Val Glu Ala Gly		
500	505	510
Met Asp Thr Leu Ile Met His Leu Cys Glu Glu Thr Ala Pro Glu Asn		
515	520	525
Gln Lys Phe Ile Leu Gln Glu Asp Gly Ser Leu Phe His Glu Gln Ser		
530	535	540
Lys Lys Cys Val Gln Ala Ala Arg Lys Glu Ser Ser Asp Ser Phe Val		
545	550	555
Pro Leu Leu Arg Asp Cys Thr Asn Ser Asp His Gln Lys Trp Phe Phe		
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Lys Glu Arg Met Leu		
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<210> 3

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<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (1)...(1746)

<400> 3

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	15

ggc cgg gag gcg ctg ttg gtg ctc ctg gcg cta ctg gcg ttg gcc ggg	96
Gly Arg Glu Ala Leu Leu Val Leu Leu Ala Leu Leu Ala Leu Ala Gly	
20	25
	30

ctg ggc tcg gtg ctg cgg gcg cag cgt ggg gcc ggg ggg gct gcc	144
Leu Gly Ser Val Leu Arg Ala Gln Arg Gly Ala Gly Ala Gly Ala Ala	
35	40
	45

gag ccg gga ccc ccg cgc acc ccg cgc ccc ggg cgg cgc gag ccg gtc	192
Glu Pro Gly Pro Pro Arg Thr Pro Arg Pro Gly Arg Arg Glu Pro Val	
50	55
	60

2007-2008

Ile Arg Ser Pro Thr Met Ala Gly Gly Leu Phe Ala Val Ser Lys				
305	310	315	320	
tat ttt gaa tat ctg ggg tct tat gat aca gga atg gaa gtt tgg gga				1008
Tyr Phe Glu Tyr Leu Gly Ser Tyr Asp Thr Gly Met Glu Val Trp Gly				
325	330	335		
gga gaa aac ctc gaa ttt tcc ttt agg atc tgg cag tgt ggt ggg gtt				1056
Gly Glu Asn Leu Glu Phe Ser Phe Arg Ile Trp Gln Cys Gly Gly Val				
340	345	350		
ctg gaa aca cac cca tgt tcc cat gtt gcc cat gtt ttc ccc aag caa				1104
Leu Glu Thr His Pro Cys Ser His Val Gly His Val Phe Pro Lys Gln				
355	360	365		
gct ccc tac tcc cgc aac aag gct ctg gcc aac agt gtt cgt gca gct				1152
Ala Pro Tyr Ser Arg Asn Lys Ala Leu Ala Asn Ser Val Arg Ala Ala				
370	375	380		
gaa gta tgg atg gat gaa ttt aaa gag ctc tac tac cat cgc aac ccc				1200
Glu Val Trp Met Asp Glu Phe Lys Glu Leu Tyr Tyr His Arg Asn Pro				
385	390	395	400	
cgt gcc cgc ttg gaa cct ttt ggg gat gtg aca gag agg aag cag ctc				1248
Arg Ala Arg Leu Glu Pro Phe Gly Asp Val Thr Glu Arg Lys Gln Leu				
405	410	415		
cg gac aag ctc cag tgt aaa gac ttc aag tgg ttc ttg gag act gtg				1296
Arg Asp Lys Leu Gln Cys Lys Asp Phe Lys Trp Phe Leu Glu Thr Val				
420	425	430		
tat cca gaa ctg cat gtg cct gag gac agg cct ggc ttc ttc ggg atg				1344
Tyr Pro Glu Leu His Val Pro Glu Asp Arg Pro Gly Phe Phe Gly Met				
435	440	445		
ctc cag aac aaa gga cta aca gac tac tgc ttt gac tat aac cct ccc				1392
Leu Gln Asn Lys Gly Leu Thr Asp Tyr Cys Phe Asp Tyr Asn Pro Pro				
450	455	460		
gat gaa aac cag att gtg gga cac cag gtc att ctg tac ctc tgt cat				1440
Asp Glu Asn Gln Ile Val Gly His Gln Val Ile Leu Tyr Leu Cys His				
465	470	475	480	
ggg atg ggc cag aat cag ttt ttc gag tac acg tcc cag aaa gaa ata				1488
Gly Met Gly Gln Asn Gln Phe Phe Glu Tyr Thr Ser Gln Lys Glu Ile				
485	490	495		
cgc tat aac acc cac cag cct gag ggc tgc att gct gtg gaa gca gga				1536
Arg Tyr Asn Thr His Gln Pro Glu Gly Cys Ile Ala Val Glu Ala Gly				
500	505	510		
atg gat acc ctt atc atg cat ctc tgc gaa gaa act gcc cca gag aat				1584
Met Asp Thr Leu Ile Met His Leu Cys Glu Glu Thr Ala Pro Glu Asn				
515	520	525		
cag aag ttc atc ttg cag gag gat gga tct tta ttt cac gaa cag tcc				1632
Gln Lys Phe Ile Leu Gln Glu Asp Gly Ser Leu Phe His Glu Gln Ser				
530	535	540		
aag aaa tgt gtc cag gct gcg agg aag gag tcg agt gac agt ttc gtt				1680
Lys Lys Cys Val Gln Ala Ala Arg Lys Glu Ser Ser Asp Ser Phe Val				

545 550 555 560

cca ctc tta cga gac tgc acc aac tcg gat cat cag aaa tgg ttc ttc
Pro Leu Leu Arg Asp Cys Thr Asn Ser Asp His Gln Lys Trp Phe Phe
565 570 575

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1728 1746

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<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus

<400> 4

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35 40 45
Glu Asp Tyr Leu Asp Glu Arg Ile Lys Glu Glu Asn Pro Arg Ile Ile
50 55 60
Ile Val Ile Arg Leu Glu Asn Ser Gln Gly Pro Ala Ala Ala Arg
65 70 75 80
Asn Lys Gly Ile Arg Arg Ala Thr Gly Asp Ser Asp Tyr Ile Leu Phe
85 90 95
Leu Asp Ala Asp Asp Ile Phe Thr Pro Asp Lys Leu Glu Lys Leu Ile
100 105 110
Asp Tyr Ala Glu Ala Thr Asp Ala Ala Val Val Leu Gly Ala Ile Asp
115 120 125
Ala Tyr Glu Tyr Ala Glu Gly Glu Ser Asn Leu Tyr Arg Ile Ala Arg
130 135 140
Ala Asp Thr Glu Arg Ser Leu Phe Ala Gly Leu Leu Arg Lys Thr Gly
145 150 155 160
Arg Leu Thr Gly Gly Leu Glu Leu Ser Phe Glu Ile Gly Ser Asn Ala
165 170 175
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1728 1746

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<211> 145
<212> PRT
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<220>
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35 40 45

Thr Tyr Asp Glu Ser Asp Gly Glu Ile Arg Ser Val Val Asn Asn Asp
50 55 60
Lys Cys Leu Thr Val Asn Ala Asn Ser Pro Gly Ser Glu Val Lys Leu
65 70 75 80
Tyr Gln Cys Asp Ser Ala Thr Ser Asp Asn Gln Lys Trp Glu Leu Asn
85 90 95
Asn Asp Gly Leu Ile Gly Asn Lys Ile Leu Leu Asn Leu Val Asn Thr
100 105 110
Gly Leu Val Leu Asp Val Lys Gly Ser Asp Thr Gln Asn Gly Thr Lys
115 120 125
Leu Ile Leu Tyr Thr Cys Ser Gly Gly Arg Asn Gln Gln Trp Leu Pro
130 135 140
Thr
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<210> 6

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus

<400> 6

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35 40 45
Glu Ser Asp Gly Ala Ile Arg Ile Asn Ser Asp Leu Cys Leu Thr Val
50 55 60
Asn Gly Thr Val Thr Leu Tyr Ser Cys Asp Gly Thr Asp Lys Gly Asn
65 70 75 80
Asp Asn Gln Lys Trp Glu Val Asn Lys Asp Gly Thr Ile Arg Asn Pro
85 90 95
Lys Asn Ser Lys Lys Gly Val Asp Ser Gly Leu Cys Leu Asp Val Lys
100 105 110
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<210> 7

<211> 166

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus

<400> 7

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20 25 30
Asn Lys Glu Tyr Phe Glu Glu Leu Gly Thr Tyr Asp Pro Gly Met Asp
35 40 45
Ile Trp Gly Gly Glu Asn Leu Glu Leu Ser Phe Arg Val Trp Gln Cys

50	55	60													
Gly	Gly	Arg	Leu	Glu	Ile	Val	Pro	Cys	Ser	His	Val	Gly	His	Val	Phe
65															80
Arg	Lys	Arg	Ser	Pro	Tyr	Thr	Phe	Pro	Gly	Lys	Gly	Ser	Gly	Lys	Asp
															95
Val	Ile	Ser	Arg	Asn	Thr	Val	Arg	Val	Ala	Glu	Val	Trp	Met	Asp	Asp
															110
Tyr	Lys	Glu	Tyr	Phe	Tyr	Lys	His	Asn	Pro	Gln	Ala	Arg	Lys	Val	Arg
															125
Asp	Phe	Gly	Asp	Ile	Ser	Glu	Arg	Lys	Glu	Leu	Arg	Glu	Lys	Leu	Gln
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Cys	Lys	Ser	Phe	Lys	Trp	Tyr	Leu	Glu	Asn	Val	Tyr	Pro	Asp	Leu	Tyr
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Val	Pro	Ala	His	Glu	Pro										
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<210> 8
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 <212> PRT
 <213> Mus musculus

<400> 8																
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Tyr	Ala	Ser	Pro	Gly	Ala	Gly	Gly	Ala	Arg	Glu	Leu	Gly	Pro	Arg	Arg	
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Leu	Pro	Asp	Leu	Asp	Thr	Arg	Glu	Glu	Asp	Leu	Ser	Gln	Pro	Leu	Tyr	
Ile	Lys	Pro	Pro	Ala	Asp	Ser	His	Ala	Leu	Gly	Glu	Trp	Gly	Arg	Ala	
65															80	
Ser	Lys	Leu	Gln	Leu	Asn	Glu	Gly	Glu	Leu	Lys	Gln	Gln	Glu	Glu	Leu	
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Ile	Glu	Arg	Tyr	Ala	Ile	Asn	Ile	Tyr	Leu	Ser	Asp	Arg	Ile	Ser	Leu	
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His	Arg	His	Ile	Glu	Asp	Lys	Arg	Met	Tyr	Glu	Cys	Lys	Ala	Lys	Lys	
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Phe	His	Tyr	Arg	Ser	Leu	Pro	Thr	Thr	Ser	Val	Ile	Ile	Ala	Phe	Tyr	
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Asn	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	Ile	His	Ser	Val	Leu	Glu	
145															160	
Thr	Ser	Pro	Ala	Val	Leu	Leu	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Leu	
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Ser	Asp	Arg	Ile	Tyr	Leu	Lys	Ala	Gln	Leu	Glu	Thr	Tyr	Ile	Ser	Asn	
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Leu	Glu	Arg	Val	Arg	Leu	Ile	Arg	Thr	Asn	Lys	Arg	Glu	Gly	Leu	Val	
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Arg	Ala	Arg	Leu	Ile	Gly	Ala	Thr	Phe	Ala	Thr	Gly	Asp	Val	Leu	Thr	
210															220	
Phe	Leu	Asp	Cys	His	Cys	Glu	Cys	Asn	Thr	Gly	Trp	Leu	Glu	Pro	Leu	
225															240	
Leu	Glu	Arg	Ile	Ser	Arg	Asp	Glu	Thr	Ala	Ile	Val	Cys	Pro	Val	Ile	
															255	
Asp	Thr	Ile	Asp	Trp	Asn	Thr	Phe	Glu	Phe	Tyr	Met	Gln	Thr	Gly	Glu	
															270	
Pro	Met	Ile	Gly	Gly	Phe	Asp	Trp	Arg	Leu	Thr	Phe	Gln	Trp	His	Ser	
															285	
Val	Pro	Lys	His	Glu	Arg	Asp	Arg	Arg	Thr	Ser	Arg	Ile	Asp	Pro	Ile	
290															300	

Arg Ser Pro Thr Met Ala Gly Gly Leu Phe Ala Val Ser Lys Lys Tyr
 305 310 315 320
 Phe Gln Tyr Leu Gly Thr Tyr Asp Thr Gly Met Glu Val Trp Gly Gly
 325 330 335
 Glu Asn Leu Glu Leu Ser Phe Arg Val Trp Gln Cys Gly Gly Lys Leu
 340 345 350
 Glu Ile His Pro Cys Ser His Val Gly His Val Phe Pro Lys Arg Ala
 355 360 365
 Pro Tyr Ala Arg Pro Asn Phe Leu Gln Asn Thr Ala Arg Ala Ala Glu
 370 375 380
 Val Trp Met Asp Glu Tyr Lys Glu His Phe Tyr Asn Arg Asn Pro Pro
 385 390 395 400
 Ala Arg Lys Glu Ala Tyr Gly Asp Leu Ser Glu Arg Lys Leu Leu Arg
 405 410 415
 Glu Arg Leu Lys Cys Lys Ser Phe Asp Trp Tyr Leu Lys Asn Val Phe
 420 425 430
 Ser Asn Leu His Val Pro Glu Asp Arg Pro Gly Trp His Gly Ala Ile
 435 440 445
 Arg Ser Met Gly Ile Ser Ser Glu Cys Leu Asp Tyr Asn Ala Pro Asp
 450 455 460
 Asn Asn Pro Thr Gly Ala Asn Leu Ser Leu Phe Gly Cys His Gly Gln
 465 470 475 480
 Gly Gly Asn Gln Phe Phe Glu Tyr Thr Ser Asn Lys Glu Ile Arg Phe
 485 490 495
 Asn Ser Val Thr Glu Leu Cys Ala Glu Val Pro Gln Gln Lys Asp Tyr
 500 505 510
 Val Gly Met Gln Asn Cys Pro Lys Asp Gly Leu Pro Val Pro Val Asn
 515 520 525
 Ile Ile Trp His Phe Lys Glu Asp Gly Thr Ile Phe His Pro His Thr
 530 535 540
 Arg Leu Cys Leu Ser Ala Tyr Arg Thr Ala Glu Gly Arg Pro Ser Val
 545 550 555 560
 His Met Lys Thr Cys Asp Ala Leu Asp Lys Asn Gln Leu Trp Arg Phe
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 Glu Lys

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<212> PRT

<213> Artificial Sequence

<220>

<223> consensus

<221> VARIANT

<222> (1)...(22)

<223> Xaa = any amino acid

<400> 9

Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa

1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu

20